

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: BROWNING, Jeffrey
WARE, Carl
- (ii) TITLE OF INVENTION: LYMPHOTOKIN-BETA, LYMPHOTOKIN-BETA
COMPLEXES, PHARMACEUTICAL PREPARATIONS AND THERAPEUTIC
USES THEREOF
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: c/o FISH & NEAVE
(B) STREET: 1251 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10020
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US91/04588
(B) FILING DATE: 27-JUN-1991
- (viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/544,862
(B) FILING DATE: 27-JUN-1990
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: HALEY Jr., James F.
(B) REGISTRATION NUMBER: 27,794
(C) REFERENCE/DOCKET NUMBER: B129CIP11

TOCOT F8204001

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (212) 596-9000
- (B) TELEFAX: (212) 596-9090
- (C) TELEX: 14-8367

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | |
|-----------------------------------------------------------------|-----|
| CIG GGG CIG GAG GGC AGG GGT GGG AGG CTC CAG GGG AGG GGT TOC CTC | 48 |
| Leu Gly Leu Glu Gly Arg Gly Gly Arg Leu Gln Gly Arg Gly Ser Leu | |
| 1 5 10 15 | |
| CIG CTA GCT GIG GCA GGA GGC ACT TCT CIG GIG ACC TTG TTG CIG GCG | 96 |
| Leu Leu Ala Val Ala Gly Ala Thr Ser Leu Val Thr Leu Leu Leu Ala | |
| 20 25 30 | |
| GIG OCT ATC ACT GTC CIG GCT GIG CIG GGC TTA GIG CCC CAG GAT CAG | 144 |
| Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro Gln Asp Gln | |
| 35 40 45 | |
| GGA GGA CIG GTA ACG GAG ACG GGC GAC CCC GGG GCA CAG GGC CAG CAA | 192 |
| Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly Ala Gln Ala Gln Gln | |
| 50 55 60 | |
| GGA CIG GGG TTT CAG AAG CIG CCA GAG GAG GAG CCA GAA ACA GAT CTC | 240 |
| Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu Pro Glu Thr Asp Leu | |
| 65 70 75 80 | |
| AGC CCC GGG CTC CCA GCT GGC CAC CTC ATA GGC GCT CCG CIG AAG GGG | 288 |
| Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro Leu Lys Gly | |
| 85 90 95 | |
| CAG GGG CTA GGC TGG GAG ACG ACG AAG GAA CAG GCG TTT CIG ACG AGC | 336 |
| Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala Phe Leu Thr Ser | |
| 100 105 110 | |
| GGG ACG CAG TTC TCG GAC GGC GAG GGG CIG GCG CTC CCG CAG GAC GGC | 384 |
| Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu Pro Gln Asp Gly | |
| 115 120 125 | |

10040221-11001

CTC TAT TAC CTC TAC TGT CTC GTC GGC TAC CGG GGC GGC GGC OCT 432
 Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly Arg Ala Pro Pro
 130 135 140

GGC GGC GGC GAC CCC CAG GGC CGC TGG GTC AGC CTG CGC AGC TCT CTG 480
 Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu Arg Ser Ser Leu
 145 150 155 160

TAC CGG GGC GGC GGC GGC TAC GGC CGC GGC ACT CCC GAG CTG CTG CTC 528
 Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro Glu Leu Leu Leu
 165 170 175

GAG GGC GGC GAG AGC GTC ACT CCA GTC CTG GAC CGC GGC AGG AGA CAA 576
 Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro Ala Arg Arg Gln
 180 185 190

GGG TAC GGC OCT CTC TGG TAC AGC AGC GTC GGC TTC GGC GGC CTG GTC 624
 Gly Tyr Gly Pro Leu Thr Tyr Thr Ser Val Gly Phe Gly Gly Leu Val
 195 200 205

CAG CTC CGG AGG GGC GAG AGG GTC TAC GTC AAC ATC AGT CAC CCC GAT 672
 Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile Ser His Pro Asp
 210 215 220

ATG GTC GAC TTC GGC AGA GGC AAG ACC TTC TTT GGC GGC GTC ATG GTC 720
 Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe Gly Ala Val Met Val
 225 230 235 240

GGG TGA 726
 Gly

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Gly Leu Glu Gly Arg Gly Gly Arg Leu Gln Gly Arg Gly Ser Leu
 1 5 10 15

Leu Leu Ala Val Ala Gly Ala Thr Ser Leu Val Thr Leu Leu Ala
 20 25 30

Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro Gln Asp Gln
 35 40 45

Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly Ala Gln Ala Gln Gln
 50 55 60

Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu Pro Glu Thr Asp Leu
65 70 75 80

Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro Leu Lys Gly
85 90 95

Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala Phe Leu Thr Ser
100 105 110

Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu Pro Gln Asp Gly
115 120 125

Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly Arg Ala Pro Pro
130 135 140

Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu Arg Ser Ser Leu
145 150 155 160

Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro Glu Leu Leu Leu
165 170 175

Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro Ala Arg Arg Gln
180 185 190

Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe Gly Gly Leu Val
195 200 205

Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile Ser His Pro Asp
210 215 220

Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe Gly Ala Val Met Val
225 230 235 240

Gly

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CIG GCC TTA GIG CCC CAG GAT CAG GGA GGA CIG GTA ACG GAG ACG GGC
Leu Ala Leu Val Pro Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala
1 5 10 15

| | |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| GAC CCG GGG GCA CAG GCC CAG CAA GGA CTG GGG TTT CAG AAG CTG CCA Asp Pro Gly Ala Gln Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro 20 25 30 | 96 |
| GAG GAG GAG CCA GAA ACA GAT CTC AGC CCG GGG CTC CCA GCT GCC CAC Glu Glu Glu Pro Glu Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His 35 40 45 | 144 |
| CTC ATA GGC GCT CCG CTG AAG GGG CAG GGG CTA GGC TGG GAG ACG ACG Leu Ile Gly Ala Pro Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr 50 55 60 | 192 |
| AAG GAA CAG GCG TTT CTG ACG AGC GGG ACG CAG TTC TCG GAC GCC GAG Lys Glu Gln Ala Phe Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu 65 70 75 80 | 240 |
| GGG CTG GCG CTC CCG CAG GAC GGC CTC TAT TAC CTC TAC TGT CTC GTC Gly Leu Ala Leu Pro Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val 85 90 95 | 288 |
| GGC TAC CCG GGC CCG GCG CCG CCG GGC GGC GGC GAC CCG CAG GGC CCG Gly Tyr Arg Gly Arg Ala Pro Pro Gly Gly Gly Asp Pro Gln Gly Arg 100 105 110 | 336 |
| TCG GTC ACG CTG CCG AGC TCT CTG TAC CCG GCG GGC GGC GGC TAC GGC Ser Val Thr Leu Arg Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly 115 120 125 | 384 |
| CCG GGC ACT CCG GAG CTG CTG CTC GAG GGC GGC GAG ACG GTC ACT CCA Pro Gly Thr Pro Glu Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro 130 135 140 | 432 |
| GTC CTG GAC CCG GGC AGG AGA CAA GGG TAC GGG OCT CTC TGG TAC ACG Val Leu Asp Pro Ala Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr 145 150 155 160 | 480 |
| AGC GTC GGC TTC GGC GGC CTG GTC CAG CTC CCG AGG GGC GAG AGG GTC Ser Val Gly Phe Gly Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val 165 170 175 | 528 |
| TAC GTC AAC ATC AGT CAC CCG GAT ATG GTC GAC TTC GCG AGA GGG AAG Tyr Val Asn Ile Ser His Pro Asp Met Val Asp Phe Ala Arg Gly Lys 180 185 190 | 576 |
| AAC TTC TTT GGG GCC GTC ATG GTC GGG TGA Thr Phe Phe Gly Ala Val Met Val Gly 195 200 | 606 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

102011-13204001

(ii) MOLECULE TYPE: protein

(xci) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Leu Ala Leu Val Pro Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala
 1             5             10             15
Asp Pro Gly Ala Gln Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro
      20             25             30
Glu Glu Glu Pro Glu Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His
      35             40             45
Leu Ile Gly Ala Pro Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr
      50             55             60
Lys Glu Gln Ala Phe Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu
      65             70             75             80
Gly Leu Ala Leu Pro Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val
      85             90             95
Gly Tyr Arg Gly Arg Ala Pro Pro Gly Gly Gly Asp Pro Gln Gly Arg
      100            105            110
Ser Val Thr Leu Arg Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly
      115            120            125
Pro Gly Thr Pro Glu Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro
      130            135            140
Val Leu Asp Pro Ala Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr
      145            150            155            160
Ser Val Gly Phe Gly Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val
      165            170            175
Tyr Val Asn Ile Ser His Pro Asp Met Val Asp Phe Ala Arg Gly Lys
      180            185            190
Thr Phe Phe Gly Ala Val Met Val Gly
      195            200

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | |
|-----------------------------------------------------------------|-----|
| CCG CIG AAG GGG CAG GGG CTA GGC TGG GAG ACG ACG AAG GAA CAG GCG | 48 |
| Pro Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala | |
| 1 5 10 15 | |
| TIT CIG ACG AGC GGG AGC CAG TTC TCG GAC GGC GAG GGG CIG GCG CTC | 96 |
| Phe Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu | |
| 20 25 30 | |
| CCG CAG GAC GGC CTC TAT TAC CTC TAC TGT CTC GTC GGC TAC CCG GCG | 144 |
| Pro Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly | |
| 35 40 45 | |
| CGG GCG CCC OCT GGC GGC GGG GAC CCC CAG GGC CGC TCG GTC ACG CIG | 192 |
| Arg Ala Pro Pro Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu | |
| 50 55 60 | |
| CGC AGC TCT CIG TAC CGG GCG GGG GGC GGC TAC GGG CGC GGC ACT CCC | 240 |
| Arg Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro | |
| 65 70 75 80 | |
| GAG CIG CIG CTC GAG GGC GGC GAG ACG GIG ACT CCA GIG CIG GAC CCG | 288 |
| Glu Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro | |
| 85 90 95 | |
| GCC AGG AGA CAA GGG TAC GGG OCT CTC TGG TAC ACG AGC GIG GGG TTC | 336 |
| Ala Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe | |
| 100 105 110 | |
| GGC GGC CIG GIG CAG CTC CGG AGG GGC GAG AGG GIG TAC GTC AAC ATC | 384 |
| Gly Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile | |
| 115 120 125 | |
| AGT CAC CCC GAT ATG GIG GAC TTC GCG AGA GGG AAG ACC TTC TTT GGG | 432 |
| Ser His Pro Asp Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe Gly | |
| 130 135 140 | |
| GCC GIG ATG GIG GGG TGA | 450 |
| Ala Val Met Val Gly | |
| 145 | |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

FBI/DOJ - T3204001

Pro Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala
 1 5 10 15
 Phe Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu
 20 25 30
 Pro Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly
 35 40 45
 Arg Ala Pro Pro Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu
 50 55 60
 Arg Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro
 65 70 75 80
 Glu Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro
 85 90 95
 Ala Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe
 100 105 110
 Gly Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile
 115 120 125
 Ser His Pro Asp Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe Gly
 130 135 140
 Ala Val Met Val Gly
 145

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | |
|-----------------------------------------------------------------|----|
| CIG GOC TTA GTG CCC CAG GAT CAG GGA GGA CIG GTA ACG GAG ACG GOC | 48 |
| Leu Ala Leu Val Pro Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala | |
| 1 5 10 15 | |
| GAC CCC GGG GCA CAG GOC CAG CAA GGA CIG GGG TTT CAG AAG CIG CCA | 96 |
| Asp Pro Gly Ala Gln Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro | |
| 20 25 30 | |

10040331-11070

GAG GAG GAG CCA GAA ACA GAT CTC AGC CCC GGG CTC CCA GCT GCC CAC 144
Glu Glu Glu Pro Glu Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His
35 40 45

CTC ATA GGC GCT 156
Leu Ile Gly Ala
50

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Ala Leu Val Pro Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala
1 5 10 15
Asp Pro Gly Ala Gln Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro
20 25 30
Glu Glu Glu Pro Glu Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His
35 40 45
Leu Ile Gly Ala
50

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHEetical: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCTGGGCT CTCCTC

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GYTONGGTT CYTCYTC

17

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGGGGGCAC TGGGGCTG

18

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

10040331.110701

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /function= "linker"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "The 5' terminal 4 nucleotides in the complementary strand are not present in this linker "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCGGCGCCT TAGAGACA

19

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GACAGTGATA GGCAAGGACA GCAACAA

27

10040331.10701